

RAW SEQUENCE LISTING

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Application Serial Number: 10/551,054
Source: PCT
Date Processed by STIC: 10/07/2005

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RAW SEQUENCE LISTING

DATE: 10/07/2005

PATENT APPLICATION: US/10/551,054

TIME: 10:18:32

Input Set : A:\Sequence Listing ascii.txt

Output Set: N:\CRF4\10072005\J551054.raw

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3 <110> APPLICANT: Bachmann, Martin
4      Manolova, Vania
5      Meijerink, Edwin
6      Proba, Karl
7      Schwarz, Katrin
9 <120> TITLE OF INVENTION: Melan-A-Carrier-Conjugates
11 <130> FILE REFERENCE: 1700.0590000
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/551,054
C--> 13 <141> CURRENT FILING DATE: 2005-09-23
13 <150> PRIOR APPLICATION NUMBER: US 60/457,348
14 <151> PRIOR FILING DATE: 2003-03-26
16 <160> NUMBER OF SEQ ID NOS: 94
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 10
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: oligonucleotide ISS
28 <400> SEQUENCE: 1
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33 <211> LENGTH: 19
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
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38 <223> OTHER INFORMATION: oligonucleotide G3-6
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44 <210> SEQ ID NO: 3
45 <211> LENGTH: 20
46 <212> TYPE: DNA
47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
50 <223> OTHER INFORMATION: oligonucleotide G4-6
52 <400> SEQUENCE: 3
53 gggggacgat cgtcggggg                             20
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 21
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: oligonucleotide G5-6

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68 <210> SEQ ID NO: 5
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70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial sequence
73 <220> FEATURE:
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80 <210> SEQ ID NO: 6
81 <211> LENGTH: 24
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: oligonucleotide G7-7
88 <400> SEQUENCE: 6
89 ggggggggac gatcgtcggg gggg 24
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 26
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: oligonucleotide G8-8
100 <400> SEQUENCE: 7
101 ggggggggga cgatcgtcgg gggggg 26
104 <210> SEQ ID NO: 8
105 <211> LENGTH: 28
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
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112 <400> SEQUENCE: 8
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117 <211> LENGTH: 30
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial sequence
121 <220> FEATURE:
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124 <400> SEQUENCE: 9
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128 <210> SEQ ID NO: 10
129 <211> LENGTH: 132
130 <212> TYPE: PRT
131 <213> ORGANISM: Bacteriophage Q-beta
133 <400> SEQUENCE: 10
135 Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Lys
136 1 5 10 15

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139 Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
140      20      25      30
143 Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
144      35      40      45
147 Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
148      50      55      60
151 Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
152 65      70      75      80
155 Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe
156      85      90      95
159 Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
160      100     105     110
163 Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
164      115     120     125
167 Asn Pro Ala Tyr
168      130
171 <210> SEQ ID NO: 11
172 <211> LENGTH: 328
173 <212> TYPE: PRT
174 <213> ORGANISM: Bacteriophage Q-beta
176 <400> SEQUENCE: 11
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182 Lys Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
183      20      25      30
186 Val Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
187      35      40      45
190 Val Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
191      50      55      60
194 Val Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser
195 65      70      75      80
198 Cys Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser
199      85      90      95
202 Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu
203      100     105     110
206 Leu Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln
207      115     120     125
210 Leu Asn Pro Ala Tyr Trp Leu Leu Ile Ala Gly Gly Gly Ser Gly Ser
211      130     135     140
214 Lys Pro Asp Pro Val Ile Pro Asp Pro Pro Ile Asp Pro Pro Pro Gly
215 145     150     155     160
218 Thr Gly Lys Tyr Thr Cys Pro Phe Ala Ile Trp Ser Leu Glu Glu Val
219      165     170     175
222 Tyr Glu Pro Pro Thr Lys Asn Arg Pro Trp Pro Ile Tyr Asn Ala Val
223      180     185     190
226 Glu Leu Gln Pro Arg Glu Phe Asp Val Ala Leu Lys Asp Leu Leu Gly
227      195     200     205
230 Asn Thr Lys Trp Arg Asp Trp Asp Ser Arg Leu Ser Tyr Thr Thr Phe
231      210     215     220

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234 Arg Gly Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp Ala Thr Tyr Leu
235 225                230                235                240
238 Ala Thr Asp Gln Ala Met Arg Asp Gln Lys Tyr Asp Ile Arg Glu Gly
239                245                250                255
242 Lys Lys Pro Gly Ala Phe Gly Asn Ile Glu Arg Phe Ile Tyr Leu Lys
243                260                265                270
246 Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His Ala
247                275                280                285
250 Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly Ala
251 290                295                300
254 Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile Gln
255 305                310                315                320
258 Ala Val Ile Val Val Pro Arg Ala
259                325
262 <210> SEQ ID NO: 12
263 <211> LENGTH: 362
264 <212> TYPE: PRT
265 <213> ORGANISM: BK virus
267 <400> SEQUENCE: 12
269 Met Ala Pro Thr Lys Arg Lys Gly Glu Cys Pro Gly Ala Ala Pro Lys
270 1                5                10                15
273 Lys Pro Lys Glu Pro Val Gln Val Pro Lys Leu Leu Ile Lys Gly Gly
274                20                25                30
277 Val Glu Val Leu Glu Val Lys Thr Gly Val Asp Ala Ile Thr Glu Val
278                35                40                45
281 Glu Cys Phe Leu Asn Pro Glu Met Gly Asp Pro Asp Asp Asn Leu Arg
282 50                55                60
285 Gly Tyr Ser Gln His Leu Ser Ala Glu Asn Ala Phe Glu Ser Asp Ser
286 65                70                75                80
289 Pro Asp Arg Lys Met Leu Pro Cys Tyr Ser Thr Ala Arg Ile Pro Leu
290                85                90                95
293 Pro Asn Leu Asn Glu Asp Leu Thr Cys Gly Asn Leu Leu Met Trp Glu
294                100               105               110
297 Ala Val Thr Val Lys Thr Glu Val Ile Gly Ile Thr Ser Met Leu Asn
298                115               120               125
301 Leu His Ala Gly Ser Gln Lys Val His Glu Asn Gly Gly Gly Lys Pro
302 130               135               140
305 Val Gln Gly Ser Asn Phe His Phe Phe Ala Val Gly Gly Asp Pro Leu
306 145               150               155               160
309 Glu Met Gln Gly Val Leu Met Asn Tyr Arg Thr Lys Tyr Pro Gln Gly
310                165                170                175
313 Thr Ile Thr Pro Lys Asn Pro Thr Ala Gln Ser Gln Val Met Asn Thr
314                180                185                190
317 Asp His Lys Ala Tyr Leu Asp Lys Asn Asn Ala Tyr Pro Val Glu Cys
318                195                200                205
321 Trp Ile Pro Asp Pro Ser Arg Asn Glu Asn Thr Arg Tyr Phe Gly Thr
322 210               215               220
325 Tyr Thr Gly Gly Glu Asn Val Pro Pro Val Leu His Val Thr Asn Thr
326 225               230               235               240

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329 Ala Thr Thr Val Leu Leu Asp Glu Gln Gly Val Gly Pro Leu Cys Lys
330           245           250           255
333 Ala Asp Ser Leu Tyr Val Ser Ala Ala Asp Ile Cys Gly Leu Phe Thr
334           260           265           270
337 Asn Ser Ser Gly Thr Gln Gln Trp Arg Gly Leu Ala Arg Tyr Phe Lys
338           275           280           285
341 Ile Arg Leu Arg Lys Arg Ser Val Lys Asn Pro Tyr Pro Ile Ser Phe
342           290           295           300
345 Leu Leu Ser Asp Leu Ile Asn Arg Arg Thr Gln Lys Val Asp Gly Gln
346 305           310           315           320
349 Pro Met Tyr Gly Met Glu Ser Gln Val Glu Glu Val Arg Val Phe Asp
350           325           330           335
353 Gly Thr Glu Gln Leu Pro Gly Asp Pro Asp Met Ile Arg Tyr Ile Asp
354           340           345           350
357 Arg Gln Gly Gln Leu Gln Thr Lys Met Val
358           355           360
361 <210> SEQ ID NO: 13
362 <211> LENGTH: 130
363 <212> TYPE: PRT
364 <213> ORGANISM: Bacteriophage fr
366 <400> SEQUENCE: 13
368 Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
369 1           5           10           15
372 Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
373           20           25           30
376 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
377           35           40           45
380 Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
381           50           55           60
384 Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
385 65           70           75           80
388 Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
389           85           90           95
392 Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
393           100          105          110
396 Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
397           115          120          125
400 Ile Tyr
401           130
404 <210> SEQ ID NO: 14
405 <211> LENGTH: 130
406 <212> TYPE: PRT
407 <213> ORGANISM: Bacteriophage GA
409 <400> SEQUENCE: 14
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412 1           5           10           15
415 Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp
416           20           25           30
419 Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date